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Nutritional characteristics of *BMR* mutant and normal sorghum genotypes used for cutting and grazing

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ABSTRACT. This study evaluated the nutritional characteristics of *BMR* mutant and normal sorghum genotypes, eleven *BMR* mutants and nine normal. Seeds were sown in a randomized block design with three blocks, in which each genotype was a treatment. The nutritional characteristics were analyzed at 42 days of regrowth after the first cut, determined for DM, EE, ash, CP, NDIN, NIDA, NDF, ADF, NFC, CT, HCEL, CEL and NGLs. Regarding DM, EE, ash, NDIN, NIDA, NDF, FDA and HCEL, there were no differences between genotypes. As for CP, there were differences, with mean levels ranging from 9.77% for BR001AXTX2785bmr to 16.45% for BR001AxTX2784. Considering CT and NFC, there were differences in the mean levels that ranged from 75.21 to 83.28% for BR007AxTX2785bmr and BR001AXTX2785bmr, and from 17.46 to 25.51% for CMSXS156AxTX2785bmr and IS10428xTX2784, respectively. In relation to CEL and LGN significant difference were detected, the mean levels varied between 22.30 and 27.94% for the IS10428xTX2784 and TX635AxTX2785bmr, and from 3.08 to 7.31% for BR007AxTX2785bmr and BR001AxTX2784, respectively. The genotypes IS10428xTX2784 and BR007AxTX2784 are the most suitable for use in ruminant feed.

Keywords: forage, isogenic, mutation, brown midrib.

Características nutricionais de genótipos de sorgo mutantes *BMR* e normais utilizados para corte e pastejo

RESUMO. Objetivou-se avaliar as características nutricionais de genótipos de sorgo mutantes *BMR* e normais, sendo onze mutantes *BMR* e nove normais. A semeadura foi realizada em blocos casualizados, com três blocos onde cada genótipo foi um tratamento. As características nutricionais foram analisadas aos 42 dias de rebrotação após o primeiro corte, sendo determinados os teores de MS, EE, cinzas, PB, NIDN, NIDA, FDN, FDA, CNF, CT, HCEL, CEL e LGN. Em relação à MS, ao EE, às cinzas, ao NIDN, ao NIDA, à FDN, à FDA e à HCEL, não houve diferença entre os genótipos. Quanto à PB, houve diferença, cujos teores médios oscilaram de 9,77% para o BR001AXTX2785bmr a 16,45% para o BR001AxTX2784. Em relação aos CT e CNF, houve diferença, os teores médios variaram de 75,21% para o BR007AxTX2785bmr a 83,28% para o BR001AXTX2785bmr e de 17,46 a 25,51% para o CMSXS156AxTX2785bmr e IS10428xTX2784, respectivamente. Quanto à CEL e LGN houve diferença, os teores médios variaram de 22,30% para o IS10428xTX2784 a 27,94% para o TX635AxTX2785bmr e de 3,08% para o BR007AxTX2785bmr a 7,31% para o BR001AxTX2784, respectivamente. Os genótipos IS10428xTX2784 e o BR007AxTX2784 são os mais indicados para se utilizar na alimentação de ruminantes.

Palavras-chave: forragem, isogênicos, mutação, nervura marron.

Introduction

In Brazil there is a marked seasonality in forage production, which makes production systems mostly dependent on the planning for use of conserved forage or forage with high drought tolerance. Sorghum has the potential to be used as ruminant feed, especially in semi-arid regions, for being resistant to drought and high temperatures, and shows high yield and high nutritional value (LIMA et al., 2005). In ruminant nutrition, sorghum can be used for producing hay, silage and for cutting and/or grazing.

The hybrids used mainly for grazing, green cutting, haying and dead mulching result from a cross between two distinct species of the genus *Sorghum*. To produce these hybrids, it is used as female a lineage of grain sorghum (*Sorghum bicolor* cv. Bicolor) and as male, a lineage of sudangrass (*Sorghum sudanense* cv. Sudanense) (RIBAS, 2008).

BMR mutant plants (brown midrib trait) are phenotypically characterized by the presence of brownish pigments on the midrib of the leaf and in the stem. These pigments are strongly associated with the lignin as they persist in the cell wall after the removal of hemicellulose and cellulose (HALPIN et al., 1998). The *BMR* phenotype is characteristic of diploid plants and may occur spontaneously in nature or be produced by genetic engineering (BARRIÉRE et al., 2004).

Mutation in sorghum was generated from chemical treatment of seeds with di-ethyl sulfide, which produced nineteen *BMR* mutants of independent occurrence identified in segregated progenies. Some of these mutants show a significant reduction in lignin content and increased cell wall digestibility. From these nineteen genes, three were selected for better agronomic traits (*bmr-6, bmr-12* and *bmr-18*) (FRITZ et al., 1988).

The *bmr-6* causes a reduction in the enzyme cinnamyl alcohol dehydrogenase (CAD) activity, while the *bmr-12* and *bmr-18* decreases the activity of the enzyme Omethyltransferase (OMT) in the lignin synthesis of the sorghum (OLIVER et al., 2005). Caster et al. (2003) studied the changes caused by the *bmr-6* mutation in two cultivars of sudangrass. The *BMR* phenotypes showed an increased nutritional value compared to normal materials, but the yield was reduced.

BMR mutant genotypes of sorghum and sudangrass have been targeted for study, given the lower lignin content and consequently higher digestibility, dry matter intake and productivity per animal. The goal of this study was to evaluate the nutritional characteristics of *BMR* mutant and normal genotypes of sorghum used for cutting and grazing.

Material and methods

The experiment was conducted at the Corn and Sorghum Research Center of Embrapa located at the Km 65 of MG 424 road in the city of Sete Lagoas, Minas Gerais State, Brazil.

The climate according to Koppen is AW (savanna climate with dry winter). The mean annual rainfall is 1,271.9 mm, with a mean annual temperature of 20.9°C and relative humidity of about 70.5% (ANTUNES, 1994). The soil is classified as Dystrophic Red typical cerrado phase (SANTOS et al., 2006).

Of the twenty genotypes used in the experiment, eleven were *BMR* mutant, carrying the bmr-6 gene for brown midrib, nine were normal. Among these genotypes, nineteen are experimental and belong to the breeding program of the Corn and Sorghum Research Center of Embrapa, and one is commercial. The experimental genotypes were composed of five isogenic pairs, distinguished by the presence (mutant) or absence (normal) of the bmr-6 gene (Table 1).

Table 1. *BMR* mutant and normal genotypes of sorghum for cutting and grazing.

Experimental Genotypes (*BMR* Mutants)	Experimental Genotypes (Normal)	Commercial Genotypes (Normal)
CMSXS156AxTX2784bmr[1]	CMSXS156AxTX2784[1]	BR 800
CMSXS156AxTX2785bmr[2]	CMSXS156AxTX2785[2]	
CMSXS157AxTX2784bmr[3]	CMSXS157AxTX2784[3]	
BR001AxTX2784bmr[4]	BR001AxTX2784[4]	
BR007AxTX2784bmr[5]	BR007AxTX2784[5]	
CMSXS157AxTX2785bmr	IS10428xTX2784	
BR007AxTX2785bmr	IS10252XTX2784	
CMSXS205AxTX2785bmr	CMSXS205AxTX2784	
TX635AxTX2785bmr		
BR001AXTX2785bmr		
TX635AxTX2784bmr		

[1, 2, 3, 4, 5]Isogenic pairs of the *BMR* mutant and normal genotypes.

The twenty genotypes were sown on December 16th, 2010, in three blocks each, consisting of 20 plots of six rows with 6 meters long and 70 centimeters between rows, 35 seeds were sown per meter in each plot, each genotype was a treatment, totaling 20 treatments.

Fertilization was performed based on soil analysis and crop requirements, in which were used 350 kg ha^{-1} of the formula 8-28-16 (N:P:K) + 0.5% zinc at sowing and 150 kg ha^{-1} topdressing urea 25 days after sowing (DAS) and soon after the first cut.

Two successive cuts were made, the first on February 3rd 2011, at 55 DAS, and the second on March 17th, 2011, at 42 days after the first cut (regrowth). Cuts were made on the two central and intermediary rows of each plot (working plot), disregarding the two external rows of each plot and 1 meter from the ends of each row (edges).

For nutritional assessment, the two middle rows of each plot were used, on the second cut at 42 days after the first. Samples were prepared with 20% of whole sorghum plants from the working area of the plot. These samples were chopped in a stationary chopper, homogenized, placed in paper bags and identified separately, soon after were weighed and then pre-dried in a forced ventilation oven at 55 °C for 72 hours. After this, the material was removed from the oven and left at room temperature for 2 hours for stabilization, and then weighed to determine the percentage of the pre-dried matter.

Pre-dried samples were taken to the Laboratory of Food Analysis, State University of Montes Claros (Unimontes), Campus Janaúba, Minas Gerais State, where they were separated and organized. The

samples were ground in a Wiley mill with 1 mm sieve, and stored in polyethylene containers for further analysis. Samples were analyzed for the contents of dry matter at 105°C according to AOAC (1980), ether extract and ash according to AOAC (1995), crude protein by determining the nitrogen content by the Kjeldahl method, according to AOAC (1980); neutral detergent insoluble nitrogen, and acid detergent insoluble nitrogen, according to Silva and Queiroz (2002), neutral detergent fiber, acid detergent fiber, hemicellulose, cellulose and lignin by the sequential method of Van Soest et al. (1991), non-fiber carbohydrates by the formula NFC = 100 - (CP + EE + ash + NDF) and total carbohydrate by the formula TC = 100 - (CP + EE + ash), according to Sniffen et al. (1992).

The experimental design was randomized blocks with 3 blocks and 20 treatments, amounting to 60 experimental plots. The means of the variables were subjected to analysis of variance using SISVAR described by Ferreira (2000) and whenever significant, treatments were compared using the Scott-Knott test at 5% probability. The statistical model is described below:

$Y_{ik} = \mu + G_i + B_k + e_{ik}$, wherein:

Y_{ik} = value observed to the genotype i, in the block k;

μ = overall mean;

G_i = effect of the genotype i, with i = 1, 2, 3, 4, 5, 6, 7, 8, 9,10 ... 20;

B_k = effect of the block k, with k = 1, 2 and 3;

e_{ik} = experimental error associated with the observed values (Y_{ik}) which by hypothesis has zero mean and variance α^2.

Results and discussion

Regarding dry matter (DM), ether extract (EE) and ash did, there were no differences between genotypes, the means were 11.87, 1.35 and 6.27%, respectively (Table 2). Sorghum genotypes for cutting and grazing are cut and/or grazed early, thus changing the effect of the *BMR* mutation, which may make it more or less significant. According to Saballos et al. (2009), the activity of *bmr* genes in sorghum is variable according to tissues and developmental stages.

The greater participation of the panicle in the physical structure of the plant is the major responsible for the change in DM content, however sorghum genotypes for cutting and grazing have very small panicles, and as they are cut and/or grazed early, panicles usually do not develop. The low availability of DM may have occurred because the genotypes have been cut at 42 regrowth days, since there is a positive correlation between physiological maturity and concentration of DM.

In accordance with NRC (1989), there is a decrease in the intake of total dry matter at 0.02% of body weight for each 1% increase in moisture in the diet from 50%. On average across genotypes examined, all had high moisture content, approximately 88%, which can reduce the consumption of this food due to rumen fill.

Table 2. Mean content of dry matter (DM), ether extract (EE), and ash in whole plants of twenty sorghum genotypes for cutting and grazing, *BMR* mutant and normal, evaluated on the second cut (data expressed as percentage of dry matter).

Genotypes	DM (%)	EE (%)	Ash (%)
CMSXS156AxTX2784bmr[1]	12.30	1.35	5.84
CMSXS156AxTX2784[1]	12.14	0.91	5.92
CMSXS156AxTX2785bmr[2]	10.99	1.64	6.74
CMSXS156AxTX2785[2]	11.54	1.39	7.39
CMSXS157AxTX2784bmr[3]	11.08	1.18	6.41
CMSXS157AxTX2784[3]	11.44	0.74	6.36
BR001AXTX2784bmr[4]	11.73	1.71	5.72
BR001AxTX2784[4]	13.71	1.52	6.37
BR007AxTX2784bmr[5]	12.47	1.50	6.51
BR007AxTX2784[5]	11.81	1.15	5.79
CMSXS157AxTX2785bmr	11.92	1.84	5.70
BR007AxTX2785bmr	11.03	1.92	7.06
CMSXS205AxTX2785bmr	11.50	1.75	6.67
TX635AxTX2785bmr	11.39	1.29	6.16
BR001AXTX2785bmr	12.41	1.07	5.88
TX635AxTX2784bmr	11.42	1.16	6.10
IS10428xTX2784	12.11	1.20	6.39
IS10252XTX2784	12.22	1.30	5.98
CMSXS205AxTX2784	12.61	1.20	5.60
BR 800	11.58	1.27	6.75
Mean	11.87	1.35	6.27
CV (%)	10.69	34.87	11.32

Means followed by different letters are significantly different by Scott-Knott test ($p < 0.05$). [1, 2, 3, 4, 5]Isogenic pairs of the *BMR* mutant and normal genotypes.

Oliveira et al. (2010) investigated normal sudangrass and forage sorghum and found mean content of 29.5 and 28.2% of DM, respectively. However, Tomich et al. (2006) and Jayme et al. (2007) evaluated several hybrids of normal sorghum with sudangrass and observed mean content of 16.7 and 16.63% DM, respectively.

According to NRC (2001), in most situations, the total fat in the diet for ruminants should not exceed 7% of DM, because it can reduce ruminal fermentation, fiber digestibility and rate of passage. In this experiment, the content values of EE were low, perhaps because it was influenced by the early cutting age.

Oliveira et al. (2010) verified a mean content of 3.80% EE in whole plants for both. Antunes et al. (2007) analyzed the chemical composition and physical parameters of 33 sorghum genotypes and registered 2.69% EE.

In relation to crude protein (CP), differences were found between genotypes. Neutral detergent insoluble nitrogen (NDIN) and acid detergent insoluble nitrogen (ADIN) were not significantly different between genotypes, mean values were 1.30 and 0.23%, respectively (Table 3).

As for crude protein (CP), values of mean content ranged from 9.77 to 16.45% for BR001AXTX2785bmr and BR001AxTX2784, respectively. The genotypes CMSXS156AxTX2785bmr, BR001AxTX2784 and BR007AxTX2785bmr showed higher contents (15.54 to 16.45%), followed by BR007AxTX2784bmr, CMSXS157AxTX2785bmr, CMSXS205AxTX2785bmr, TX635AxTX2785bmr and TX635AxTX2784bmr with intermediate contents (14.54 to 15.14%). The isogenic genotypes CMSXS156AxTX2785bmr (15.54%), BR001AxTX2784 (16.45%) and BR007AxTX2784bmr (14.85%) presented higher contents compared to their normal pairs.

Table 3. Mean content of crude protein (CP), neutral detergent insoluble nitrogen (NDIN), acid detergent insoluble nitrogen (ADIN) of whole plants of twenty sorghum genotypes for cutting and grazing, *BMR* mutant and normal, evaluated at the second cut (data in percentage of dry matter)

Genotypes	CP (%)	NDIN (%)	ADIN (%)
CMSXS156AxTX2784bmr[1]	12.98 C	1.50	0.23
CMSXS156AxTX2784[1]	13.86 C	1.30	0.24
CMSXS156AxTX2785bmr[2]	15.54 A	1.45	0.19
CMSXS156AxTX2785[2]	13.34 C	1.45	0.23
CMSXS157AxTX2784bmr[3]	14.25 C	1.32	0.22
CMSXS157AxTX2784[3]	14.07 C	1.20	0.22
BR001AXTX2784bmr[4]	13.59 C	1.24	0.26
BR001AxTX2784[4]	16.45 A	1.04	0.26
BR007AxTX2784bmr[5]	14.85 B	1.40	0.23
BR007AxTX2784[5]	12.66 C	1.14	0.21
CMSXS157AxTX2785bmr	14.59 B	1.08	0.22
BR007AxTX2785bmr	15.80 A	1.45	0.26
CMSXS205AxTX2785bmr	14.92 B	1.37	0.24
TX635AxTX2785bmr	14.54 B	1.47	0.24
BR001AXTX2785bmr	9.77 E	1.15	0.19
TX635AxTX2784bmr	15.14 B	1.34	0.26
IS10428xTX2784	9.78 E	1.05	0.22
IS10252XTX2784	13.99 C	1.36	0.22
CMSXS205AxTX2784	11.96 D	1.29	0.19
BR 800	13.44 C	1.38	0.23
Mean	13.78	1.30	0.23
CV (%)	5.55	21.69	19.09

Means followed by different letters in the column are significantly different by Scott-Knott test ($p < 0.05$). [1, 2, 3, 4, 5]Isogenic pairs of the *BMR* mutant and normal genotypes.

The high values of crude protein content found in the genotypes are related to the cutting age. In the early development of the plant, the highest concentration of protein occurs in the leaves, which explains the high content. Nevertheless, there is a decrease in protein content with physiological maturity of the plant

The genotypes showed high content of CP, which are ideal for meeting the nitrogen requirements of the rumen flora and for a good functioning of the rumen, which is at least 7%. The results of this study characterize sorghum genotypes for cutting and grazing as high-quality protein forage. This characteristic is advantageous, since one of the major problems of pastures is protein deficiency, especially in the dry season, and this plant can be an alternative to minimize this problem and reduce supplementation costs.

Penna et al. (2010) studied the nutritional value of normal hybrids of sorghum with sudangrass evaluated at three cuttings and two sowing dates, and observed mean values of 18.12 and 17.96% CP in the first and second cuts, in the first sowing. Meantime, Jayme et al. (2007) and Oliveira et al. (2010) examined normal sorghum-sudangrass hybrid, and found mean values of 7.47 and 6.8% CP, respectively.

Van Soest (1994) suggested as normal the ADIN content within the range 3-15% of total nitrogen.

For neutral detergent fiber (NDF) and acid detergent fiber (ADF) there were no differences between genotypes, the mean values were 58.08 and 35.28%, respectively. In relation to non-fiber carbohydrate and total carbohydrate, significant differences were detected between genotypes (Table 4).

Table 4. Mean content of neutral detergent fiber (NDF), acid detergent fiber (ADF), non-fiber carbohydrate (NFC) and total carbohydrates (TC) of whole plants of twenty sorghum genotypes for cutting and grazing, *BMR* mutant and normal, evaluated at the second cut (data in percentage of dry matter).

Genotypes	NDF (%)	ADF (%)	NFC (%)	TC (%)
CMSXS156AxTX2784bmr[1]	59.13	36.80	20.69 B	79.82 B
CMSXS156AxTX2784[1]	56.40	33.84	22.92 A	79.32 C
CMSXS156AxTX2785bmr[2]	58.61	36.40	17.46 B	76.08 D
CMSXS156AxTX2785[2]	58.14	35.21	19.75 B	77.88 C
CMSXS157AxTX2784bmr[3]	58.01	36.26	20.15 B	78.16 C
CMSXS157AxTX2784[3]	59.51	36.20	19.32 B	78.84 C
BR001AXTX2784bmr[4]	57.11	35.08	21.45 B	78.97 C
BR001AxTX2784[4]	57.52	34.84	18.46 B	75.57 D
BR007AxTX2784bmr[5]	57.96	34.65	19.17 B	77.13 D
BR007AxTX2784[5]	60.43	36.33	19.97 B	80.40 B
CMSXS157AxTX2785bmr	59.18	36.08	18.69 B	77.88 C
BR007AxTX2785bmr	55.88	32.40	19.32 B	75.21 D
CMSXS205AxTX2785bmr	57.93	35.87	18.73 B	76.66 D
TX635AxTX2785bmr	58.10	35.30	19.91 B	78.01 C
BR001AXTX2785bmr	59.85	36.85	23.43 A	83.28 A
TX635AxTX2784bmr	57.73	35.03	19.87 B	77.60 C
IS10428xTX2784	57.12	35.23	25.51 A	82.63 A
IS10252XTX2784	59.76	36.36	18.97 B	78.73 C
CMSXS205AxTX2784	55.98	33.62	25.26 A	81.25 B
BR 800	55.96	33.33	22.58 A	78.54 C
Mean	58.08	35.28	20.58	78.58
CV (%)	3.63	5.49	10.27	1.54

Means followed by different letters in the column are significantly different by Scott-Knott test ($p < 0.05$). [1, 2, 3, 4, 5]Isogenic pairs of the *BMR* mutant and normal genotypes.

For non-fiber carbohydrate, values of mean content ranged between 17.46 and 25.51% in CMSXS156AxTX2785bmr and IS10428xTX2784, respectively. The genotypes CMSXS156AxTX2784, BR001AXTX2785bmr, IS10428xTX2784, CMSXS205AxTX2784 and BR 800 showed higher contents (22.58 to 25.51%). The isogenic normal genotype CMSXS156AxTX2784 (22.92%) had a higher content compared to its mutant pair.

The contents of NFC not were influenced by cutting age, however there is a content decreases with advanced maturity.

In relation to total carbohydrates, the mean content varied from 75.21 to 83.28% in BR007AxTX2785bmr

and BR001AXTX2785bmr, respectively. The genotypes BR001AXTX2785bmr and IS10428xTX2784 presented higher contents (83.28 and 82.63%), followed by CMSXS156AxTX2784bmr, BR007AxTX2784 and CMSXS205AxTX2784 with intermediate contents (79.82 to 81.25%). The isogenic genotypes CMSXS156AxTX2784bmr (79.82%), CMSXS156A xTX2785 (77.88%), BR001AXTX2784bmr (78.97%) and BR007AxTX2784 (80.40%) presented higher content than their normal pairs.

High contents of total carbohydrates observed in the genotypes BR001AXTX2785bmr (83.28%), IS10428xTX2784 (82.63%) and CMSXS205A xTX2784 (81.25%) are associated with their lower contents of CP, which contributed to the highest levels of total carbohydrates.

With regard to hemicellulose (HCEL), there were no differences between genotypes, the mean was 22.73%. As for cellulose (CEL) and lignin (LGN) differences were found between genotypes (Table 5).

Table 5. Mean content of hemicellulose (HCEL), cellulose (CEL) and lignin (LGN) of whole plants of twenty sorghum genotypes for cutting and grazing, *BMR* mutant and normal, evaluated at the second cut (data in percentage of dry matter).

Genotypes	HCEL (%)	CEL (%)	LGN (%)
CMSXS156AxTX2784bmr[1]	22.33	24.86 B	4.33 B
CMSXS156AxTX2784[1]	22.56	22.80 B	5.14 B
CMSXS156AxTX2785bmr[2]	22.21	23.74 B	4.18 B
CMSXS156AxTX2785[2]	22.93	25.97 A	6.65 A
CMSXS157AxTX2784bmr[3]	21.75	26.03 A	5.10 B
CMSXS157AxTX2784[3]	23.31	25.57 A	5.74 A
BR001AXTX2784bmr[4]	22.43	24.89 B	5.64 A
BR001AxTX2784[4]	22.27	24.93 B	7.31 A
BR007AxTX2784bmr[5]	23.31	25.93 A	3.08 B
BR007AxTX2784[5]	24.10	24.58 B	5.70 A
CMSXS157AxTX2785bmr	23.11	23.89 B	4.65 B
BR007AxTX2785bmr	23.49	22.88 B	5.66 A
CMSXS205AxTX2785bmr	22.06	23.85 B	4.50 B
TX635AxTX2785bmr	22.80	27.94 A	6.56 A
BR001AXTX2785bmr	23.00	24.13 B	6.27 A
TX635AxTX2784bmr	22.71	23.63 B	6.28 A
IS10428xTX2784	21.89	22.30 B	3.89 B
IS10252XTX2784	23.41	27.89 A	5.04 B
CMSXS205AxTX2784	22.36	23.79 B	3.58 B
BR 800	22.63	24.22 B	5.78 A
Mean	22.73	24.69	5.25
CV (%)	5.56	6.19	16.90

Means followed by different letters in the column are significantly different by Scott-Knott test ($p < 0.05$). [1, 2, 3, 4, 5]Isogenic pairs of the *BMR* mutant and normal genotypes.

For cellulose, the mean contents varied from 22.30 to 27.94% in IS10428xTX2784 and TX635AxTX2785bmr, respectively. The genotypes CMSXS156AxTX2784bmr, CMSXS156AxTX2784, CMSXS156AxTX2785bmr, BR001AxTX2784bmr, BR001AXTX2784, BR007AxTX2784, CMSXS157A xTX2785bmr, BR007AxTX2785bmr, CMSXS205Ax TX2785bmr, BR001AXTX2785bmr, TX635Ax TX2784bmr, IS10428xTX2784, CMSXS205Ax TX2784 and BR 800 showed lower values (22.30 to 24.93%). The isogenic genotypes CMSXS156Ax TX2785bmr (23.74%) and BR007AxTX2784 (24.58%) presented lower contents than their normal pairs.

In turn, the mean contents of lignin ranged between 3.08 and 7.31%, in BR007AxTX2785bmr and BR001AxTX2784, respectively. The genotypes CMSXS156AxTX2784bmr, CMSXS156AxTX2784, CMSXS156AxTX2785bmr, CMSXS157AxTX2784bmr, BR007AxTX2784bmr, CMSXS157AxTX2785bmr, CMSXS205AxTX2785bmr, IS10428xTX2784, IS10252XTX2784 and CMSXS205AxTX2784 exhibited lower values (3.08 to 5.14%). The isogenic mutant pairs CMSXS156AxTX2785bmr (4.18%), CMSXS157AxTX2784bmr (5.10%) and BR007AxTX2784bmr (3.08%) showed lower values when compared to their normal pairs.

Most *BMR* mutant genotypes and isogenic *BMR* mutants showed the lowest contents of cellulose and lignin. The mutation has an effect on cellulose, but is more intense in lignin. The reduction in lignin is expected due the presence of the *bmr-6* gene that inhibits the activity of CAD (cinnamyl alcohol dehydrogenase) involved in its synthesis.

Brown midrib (*BMR*) mutant plants evidence the importance of genetic selection to improve the digestibility of forages. In studies with mutant plants, it was observed that, despite their lower agronomic value, the genotype had lower content of lignin and cellulose and higher digestibility, intake and productivity per animal (OLIVER et al., 2004).

Conclusion

The genotypes IS10428xTX2784 and BR007AxTX2784, according to nutritional characteristics evaluated, are the most suitable for use in ruminant feed. The normal genotype IS10428xTX2784 has high content of total carbohydrate and non-fiber carbohydrate, low content of cellulose and lignin. The isogenic genotype BR007AxTX2784 presents higher content of total carbohydrate and lower content of cellulose in relation to its mutant pair.

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